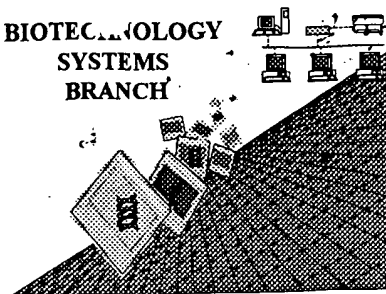


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/909,474

Source: OLP

Date Processed by STIC: 7/27/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/909,474

DATE: 07/27/2001

TIME: 10:39:06

Input Set : A:\PTO\_VSK.txt

Output Set: N:\CRF3\07272001\I909474.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: John Boylan, *surname goes first*  
 5 Alex Bowers,  
 7 <120> TITLE OF INVENTION: Novel Serine Threonine Kinase Member, h2520-59  
 9 <130> FILE REFERENCE: 01017/36524A  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/909,474  
 C--> 11 <141> CURRENT FILING DATE: 2001-07-19  
 11 <150> PRIOR APPLICATION NUMBER: US 60/219,204  
 12 <151> PRIOR FILING DATE: 2000-07-19  
 E--> 14 <160> NUMBER OF SEQ ID NOS: (12) 15 (see below)  
 16 <170> SOFTWARE: PatentIn version 3.0

## ERRORED SEQUENCES

644 <210> SEQ ID NO: 15  
 645 <211> LENGTH: 25  
 646 <212> TYPE: PRT  
 647 <213> ORGANISM: Homo sapiens  
 649 <400> SEQUENCE: 15  
 651 Arg Ser His Leu Trp Glu Ala Ala Gln Val Val Pro Asp Gly Leu Gly  
 652 1 5 10 15  
 654 Leu Asp Glu Ala Arg Glu Glu Glu Cys  
 655 20 25  
 E--> 661 (-3-) delete

see p. 2

FYI

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

<210> 5  
<211> 11  
<212> PRT  
<213> Artificial

<220>

<223> Artificial = PCR Primer

? This is an amino acid sequence.

<400> 5

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
1 5 10

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/909,474

DATE: 07/27/2001

TIME: 10:39:08

Input Set : A:\PTO\_VSK.txt

Output Set: N:\CRF3\07272001\I909474.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:269 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:282 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:295 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:310 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:324 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:449 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9  
L:449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:452 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9  
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:661 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15  
L:14 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (12) Counted (15)